

=> d his

(FILE 'HOME' ENTERED AT 10:43:45 ON 20 APR 2001)

FILE 'MEDLINE' ENTERED AT 10:44:45 ON 20 APR 2001

L1 9 S METHYLTRANSFERASE# AND ZINC-FINGER/AB,BI
L2 1 S L1 AND (FUSION OR CHIMER?)/AB,BI

FILE 'MEDLINE, EMBASE, BIOSIS, INPADOC, CAPLUS' ENTERED AT 10:45:56 ON

20

APR 2001

L3 11 S L2
L4 8 DUP REM L3 (3 DUPLICATES REMOVED)
L5 337 S METHYLTRANSFERASE# AND DNA BINDING PROTEIN#/AB,BI
L6 41 S L5 AND (FUSION OR CHIMER?)/AB,BI
L7 30 DUP REM L6 (11 DUPLICATES REMOVED)
L8 22 S L6 AND (TARGET? OR SPECIFIC?)/AB,BI
L9 18 DUP REM L8 (4 DUPLICATES REMOVED)

L9 ANSWER 16 OF 18 CAPLUS COPYRIGHT 2001 ACS
 AN 1992:485813 CAPLUS
 DN 117:85813
 TI Activation of mammalian DNA **methyltransferase** by cleavage of a
 zinc binding regulatory domain
 AU Bestor, Timothy H.
 CS Lab. Hum. Reprod. Biol., Harvard Med. Sch., Boston, MA, 02115,
 USA
 SO EMBO J. (1992), 11(7), 2611-17
 CODEN: EMJODG; ISSN: 0261-4189
 DT Journal
 LA English
 AB Mammalian DNA (cytosine-5) **methyltransferase** contains a
 C-terminal domain that is closely related to bacterial cytosine-5
 restriction **methyltransferases**. This **methyltransferase**
 domain is linked to a large N-terminal domain. It is shown here that the
 N-terminal domain contains a Zn-binding site and that the N- and
 C-terminal domains can be sepd. by cleavage with trypsin or
 Staphylococcus
 aureus protease V8; the protease V8 cleavage site was detd. by Edman
 degrdn. to lie 10 residues C-terminal of the run of alternating lysyl and
 glycyI residues which joins the two domains and six residues N-terminal
 of
 the first sequence motif conserved between the mammalian and bacterial
 cytosine **methyltransferases**. While the intact enzyme had little
 activity on unmethylated DNA substrates, cleavage between the domains
 caused a large stimulation of the initial velocity of methylation of
 unmethylated DNA without substantial change in the rate of methylation of
 hemimethylated DNA. These findings indicate that the N-terminal domain
 of
 DNA **methyltransferase** ensures the clonal propagation of
 methylation patterns through inhibition of the de novo activity of the
 C-terminal domain. Mammalian DNA **methyltransferase** is likely to
 have arisen via **fusion** of a prokaryotic-like restriction
methyltransferase and an unrelated **DNA binding**
protein. Stimulation of the de novo activity of DNA
methyltransferase by proteolytic cleavage in vivo may contribute
 to the process of ectopic methylation obsd. in the DNA of aging animals,
 tumors and in lines of cultured cells.